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SWISS-PROT: O60214

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ID TRT2_HUMAN STANDARD; PRT; 297 AA.
 AC P45379; Q99596; Q99597; O60214;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Troponin T, cardiac muscle isoforms (TnTC).
 GN .TNNT2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 6).
 RC TISSUE=Heart;
 RX MEDLINE=93345675; PubMed=8344420; [NCBI, ExPASy, EBI, Israel, Japan]
 RA Mesnard L., Samson F., Espinasse I., Durand J., Neveux J.-Y.,
 RA Mercadier J.-J.;
 RT "Molecular cloning and developmental expression of human cardiac
 troponin T.";
 RL FEBS Lett. 328:139-144(1993).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 6).
 RC TISSUE=Heart muscle;
 RX MEDLINE=94375053; PubMed=8088824; [NCBI, ExPASy, EBI, Israel, Japan]
 RA Townsend P.J., Farza H., Macgeoch C., Spurr N.K., Wade R.,
 RA Gahlman R., Yacoub M.H., Barton P.J.R.;
 RT "Human cardiac troponin T: identification of fetal isoforms and
 assignment of the TNNT2 locus to chromosome 1q.";
 RL Genomics 21:311-316(1994).
 RN [3]
 RP SEQUENCE FROM N.A. (SPLICED ISOFORMS).
 RC TISSUE=Fetal heart;
 RX MEDLINE=96129582; PubMed=8576938; [NCBI, ExPASy, EBI, Israel, Japan]
 RA Townsend P.J., Barton P.J.R., Yacoub M.H., Farza H.;
 RT "Molecular cloning of human cardiac troponin T isoforms: expression in
 developing and failing heart.";
 RL J. Mol. Cell. Cardiol. 27:2223-2236(1995).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 6; 7 AND 8).
 RC TISSUE=Heart;
 RX MEDLINE=95202803; PubMed=7534662; [NCBI, ExPASy, EBI, Israel, Japan]
 RA Anderson P.A., Greig A., Mark T.M., Malouf N.N., Oakeley A.E.,
 RA Ungerleider R.M., Allen P.D., Kay B.K.;
 RT "Molecular basis of human cardiac troponin T isoforms expressed in
 the developing, adult, and failing heart.";
 RL Circ. Res. 76:681-686(1995).
 RN [5]

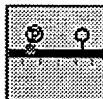
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6 AND 10).
RC TISSUE=Fetal heart;
RX MEDLINE=95202804; PubMed=7895342; [NCBI, ExPASy, EBI, Israel, Japan]
RA Mesnard L., Logeart D., Taviaux S., Diriong S., Mercadier J.-J.,
RA Samson F.;
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RP SEQUENCE FROM N.A. (ISOFORM 6), AND VARIANT FHC ILE-119.
RC TISSUE=Heart muscle;
RX MEDLINE=98141687; PubMed=9482583; [NCBI, ExPASy, EBI, Israel, Japan]
RA Gerull B., Osterziel K.-J., Witt C., Dietz R., Thierfelder L.;
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RT familial hypertrophic cardiomyopathy.";
RL Hum. Mutat. 11:179-182(1998).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM 6).
RA D'Cruz L.G., Oberoi J., Mughal F., Steffensen U., Steffensen M.,
RA Kubo T., Mogensen J., McKoy G., O'Donnoghue A., Pondel M.,
RA McKenna W.J., Carter N.D., Baboonian C.;
RT "Genomic organization of the human cardiac troponin T gene (TNNT2) and
RT characterization of the candidate promoter region.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
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RP SEQUENCE OF 190-228 AND 230-287 FROM N.A.
RC TISSUE=Blood;
RA Farza H., Townsend P.J.;
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RN [9]
RP SEQUENCE OF 69-75 AND 176-181.
RC TISSUE=Heart;
RX MEDLINE=96007936; PubMed=7498159; [NCBI, ExPASy, EBI, Israel, Japan]
RA Kovalyov L.I., Shishkin S.S., Efimochkin A.S., Kovalyova M.A.,
RA Ershova E.S., Egorov T.A., Musalyamov A.K.;
RT "The major protein expression profile and two-dimensional protein
RT database of human heart.";
RL Electrophoresis 16:1160-1169(1995).
RN [10]
RP VARIANTS FHC ASN-88 AND GLN-101.
RX MEDLINE=94265260; PubMed=8205619; [NCBI, ExPASy, EBI, Israel, Japan]
RA Thierfelder L., Watkins H., Macrae C., Lamas R., McKenna W.,
RA Vosberg H.-P., Seidman J.G., Seidman C.E.;
RT "Alpha-tropomyosin and cardiac troponin T mutations cause familial
RT hypertrophic cardiomyopathy: a disease of the sarcomere.";
RL Cell 77:701-712(1994).
RN [11]
RP VARIANTS FHC.
RX MEDLINE=95206332; PubMed=7898523; [NCBI, ExPASy, EBI, Israel, Japan]
RA Watkins H., McKenna W.J., Thierfelder L., Suk H.J., Anan R.,
RA O'Donoghue A., Spirito P., Matsumori A., Moravec C.S., Seidman J.G.,
RA Seidman C.E.;
RT "Mutations in the genes for cardiac troponin T and alpha-tropomyosin
RT in hypertrophic cardiomyopathy.";
RL New Engl. J. Med. 332:1058-1064(1995).
RN [12]
RP VARIANT FHC PRO-287.
RA Erdmann J., Wischke S., Kallisch H., Riedel K., Heidenreich M.,
RA Fleck E., Regitz-Zagrosek V.;
RT "A novel missense Arg 278 Pro mutation in the troponin T gene

RT (TNNT2).";
 RL Hum. Mutat. 12:364-364(1998).
 RN [13]
 RP VARIANT FHC LEU-103.
 RX MEDLINE=99457222; PubMed=10525521; [NCBI, ExPASy, EBI, Israel, Japan]
 RA Varnava A., Baboonian C., Davison F., de Cruz L., Elliott P.M.,
 RA Davies M.J., McKenna W.J.;
 RT "A new mutation of the cardiac troponin T gene causing familial
 hypertrophic cardiomyopathy without left ventricular hypertrophy.";
 RL Heart 82:621-624(1999).
 CC -!- FUNCTION: TROPONIN T IS THE TROPOMYOSIN-BINDING SUBUNIT OF
 CC TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS
 CC CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
 CC -!- ALTERNATIVE PRODUCTS: At least 10 isoforms; isoform 1/TNT1 (shown
 CC here), 2, 3, 4, 5, 6/TNT3, 7/TNT4, 8/TNT2, 9 and 10; may be
 CC produced by alternative splicing.
 CC -!- TISSUE SPECIFICITY: Heart. The fetal heart shows a greater
 CC expression in the atrium than in the ventricle, while the adult
 CC heart shows a greater expression in the ventricle than in the
 CC atrium. Isoform 6 predominates in normal adult heart. Isoforms 1,
 CC 7 and 8 are expressed in fetal heart. Isoform 7 is also expressed
 CC in failing adult heart.
 CC -!- DISEASE: DEFECTS IN TNNT2 ARE ONE OF THE CAUSES OF FAMILIAL
 CC HYPERTROPHIC CARDIOMYOPATHY (FHC) WHICH IS AN AUTOSOMAL DOMINANT
 CC DISORDER CHARACTERIZED BY INCREASED MYOCARDIAL MASS WITH MYOCYTE
 CC AND MYOFIBRILLAR DISARRAY. THIS FORM OF FHC IS KNOWN AS CMH2.
 CC IT IS A DISEASE OF THE SARCOMERE.
 CC -!- SIMILARITY: BELONGS TO THE TROPONIN T FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
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 DR EMBL; S64668; AAB27731.1; ALT_SEQ. [EMBL / GenBank / DDBJ] [CoCodingSequence]
 DR EMBL; X74819; CAA52818.1; -. [EMBL / GenBank / DDBJ] [CoCodingSequence]
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 DR Genew; HGNC:11949; TNNT2.
 DR MIM; 191045; -. [NCBI / EBI]
 DR GeneCards; TNNT2.
 DR GeneLynx; TNNT2.
 DR Ensembl; P45379. [Entry / Contig view]
 DR SOURCE; TNNT2.
 DR MIM; 115195; -. [NCBI / EBI]
 DR InterPro; IPR001978; Troponin.
 DR InterPro; Graphical view of domain structure.
 DR Pfam; PF00992; Troponin; 1.
 DR ProDom [Domain structure / List of seq. sharing at least 1 domain]
 DR BLOCKS; O60214.
 DR ProtoNet; O60214.
 DR ProtoMap; O60214.
 DR PRESAGE; P45379.
 DR DIP; P45379.
 DR ModBase; P45379.
 DR SWISS-2DPAGE; GET REGION ON 2D PAGE.
 KW Muscle protein; Alternative splicing; Multigene family;
 KW Phosphorylation; Disease mutation; Polymorphism; Cardiomyopathy.
 FT INIT_MET 0 0
 FT MOD_RES 1 1 PHOSPHORYLATION (BY CK2) (BY SIMILARITY).
 FT VARSPLIC 17 21 MISSING (IN ISOFORM 8).
 FT VARSPLIC 17 31 MISSING (IN ISOFORM 7).
 FT VARSPLIC 22 31 MISSING (IN ISOFORM 6).
 FT VARSPLIC 22 22 MISSING (IN ISOFORM 2 AND ISOFORM 4).
 FT VARSPLIC 53 53 MISSING (IN ISOFORM 3 AND ISOFORM 4).
 FT VARSPLIC 98 136 MISSING (IN ISOFORM 9).
 FT VARSPLIC 200 200 MISSING (IN ISOFORM 5).
 FT VARSPLIC 200 202 MISSING (IN ISOFORM 10).
 FT VARIANT 88 88 I -> N (IN FHC CMH2).
 FT VARIANT 101 101 /FTId=VAR_007605.
 FT VARIANT 103 103 R -> Q (IN FHC CMH2).
 FT VARIANT 103 103 /FTId=VAR_007606.
 FT VARIANT 119 119 R -> L (IN FHC CMH2).
 FT VARIANT 119 119 /FTId=VAR_009194.
 FT VARIANT 138 138 F -> I (IN FHC CMH2).
 FT VARIANT 138 138 /FTId=VAR_007607.
 FT VARIANT 169 169 R -> K.
 FT VARIANT 169 169 /FTId=VAR_013021.
 FT VARIANT 172 172 MISSING (IN FHC CMH2).
 FT VARIANT 172 172 /FTId=VAR_007608.
 FT VARIANT 248 248 E -> K (IN FHC CMH2).
 FT VARIANT 248 248 /FTId=VAR_007609.
 FT VARIANT 253 253 S -> T.
 FT VARIANT 253 253 /FTId=VAR_013022.
 FT VARIANT 262 262 E -> D (IN FHC CMH2).
 FT VARIANT 262 262 /FTId=VAR_007610.
 FT VARIANT 287 287 K -> R.
 FT VARIANT 287 287 /FTId=VAR_007611.
 FT VARIANT 287 287 R -> C (IN FHC CMH2).
 FT VARIANT 287 287 /FTId=VAR_007612.
 FT VARIANT 287 287 R -> P (IN FHC CMH2).
 FT VARIANT 287 287 /FTId=VAR_007613.
 FT CONFLICT 241 241 K -> E (IN REF. 8).
 FT CONFLICT 262 262 K -> R (IN REF. 8).

SQ SEQUENCE 297 AA; 35792 MW; 66FDCCD1EE4A3C965 CRC64;
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ARKKKALSNM MHFGGYIQKQ AQTERKSGKR QTEREKKKKI LAERRKVLAI DHLNEDQLRE
KAKELWQSIY NLEAEKFDLQ EFKQQKYEI NVLRNRINDN QKVSKTRGKA KVTGRWK

//

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ProDom Release 2001.3 Domain PD015088	 Graphic representation of all proteins containing this domain.  Display the family as a tree. MSF Alignment in MSF format. Build an ESPript view 
	Run Predict Protein server with this domain 

Most frequent protein names	TRT2(7)
Commentary (automatic)	MUSCLE TROPONIN CARDIAC SKELETAL PHOSPHORYLATION ISOFORMS SPLICING ALTERNATIVE FAMILY
Alignment length	72
Number of domains in family	23
Consistency indicator	DIAMETER: 124 PAM RADIUS OF GYRATION: 38 PAM SEQUENCE CLOSEST TO CONSENSUS: TRT2_BOVIN 58-107 (distance: 16 PAM)

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 [Blast Form](#)

 [References](#)

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Other descriptions of the family corresponding to this alignment



Sequence ID	start	end	weight	Sequence
1 Q13096_SALTR	42	104	4.27EETPAEEASGETQDSKAKP-KSFMPNVAPPKLPEGDGKVDFDDLHR
5 TRT1_HUMAN	.	.	2.27REERPKPSRPVVPPLIPPKIPEGE-RVDFDDIHR
4 TRT2_RAT	.	.	2.01	VEEVGPDEEAKDAEEGPVEDTKPKPSRLFMPNLVPPKI PDGE-RVDFDDIHR
8 TRT2_HUMAN	.	.	4.25EEGDREQEPGPGEESKPKPPIPMPNLVPPKI PDGE-RVDFDDIHR
2 Q93376_SALSA	.	.	3.03EQHFEEEKPK---FKPTAKAPKI PDGE-KVDFDDIQQ
1 Q99L89_MOUSE	60	93	0.30PKIPEGE-KVDFDDIQQ
1 Q9QZ47_MOUSE	59	92	0.45PKIPEGE-KVDFDDIQQ
1 Q25148_HALRO	3	63	6.42GEEEEPQQHHEDVEKP-MPRHSTTSI PRLPDGE-KVDLDVITQ
23 Consensus			23.00	VEEVGPPEETGEEEEPGQHHEDKPKPSSRPFMPNLAPPKIPDGEKGKVDFDDIHR

Minimal distance between sequences (in PAM)

20

Maximal number of clusters

12

If possible, clusterIDs should contain the following string (e.g.: human)

To display a new alignment with these parameters,
or click [here](#) to display all sequences in the family

Eukaryotic subfamily root	Bacterial subfamily root	Archaeal subfamily root	Viral subfamily root	Root of a subfamily that goes across domains of life
---------------------------	--------------------------	-------------------------	----------------------	--

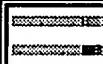
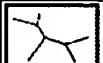
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ProDom Release 2001.3 Domain PD349636	 Graphic representation of all proteins containing this domain.  Display the family as a tree. MSF Alignment in MSF format. Build an ESPript view  Run Predict Protein server with this domain 
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Most frequent protein names	TRT2(6) TRT3(5)
Commentary (automatic)	MUSCLE TROPONIN SKELETAL PHOSPHORYLATION FAST MULTIGENE FAMILY ISOFORMS SPLICING
Alignment length	32
Number of domains in family	32
Consistency indicator	DIAMETER: 35 PAM RADIUS OF GYRATION: 14 PAM SEQUENCE CLOSEST TO CONSENSUS: Q9QUP7_MOUSE 88-117 (distance: 7 PAM)

● InterPro

ID	Accession number
"Troponin"	IPR001978

Pfam-A

ID	Accession number
Troponin	PF00992

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● [Query Form](#)

● [Blast Form](#)

● [References](#)

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Other descriptions of the family
corresponding to this alignment



Sequence ID	start	end	weight	10	20	30
2 TRT2_CHICK				7.39	EHRKKEEEELISLKDRIEQRRAERAEQQRIRS	
10 TRT2_HUMAN				6.60	ENRKKEEEELVSLKDRIEKRRRAERAEQQRIRN	
14 TRT3_RAT				5.54	EARKKEEEELVALKERIEKRRAERAEQQRIRA	
1 Q9I8U9_BRARE	57	88		5.00	EHRQKEEEELIALRERIEKRRSERAEQQRIRT	
5 TRT1_HUMAN				7.45	RKKKEEEELVALKDRIERRSERAEQQRFRT	
32 Consensus				31.98	EHRKKEEEELIALKDRIEKRRAERAEQQRIRT	

Minimal distance between sequences (in PAM)

20

Maximal number of clusters

12

If possible, clusterIDs should contain the following string (e.g.: human)

To display a new alignment with these parameters,
or click [here](#) to display all sequences in the family

Eukaryotic
subfamily root

Bacterial
subfamily root

Archaeal
subfamily root

Viral
subfamily
root

Root of a subfamily that
goes across domains of life

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General information about the entry

Entry name	TRT2_HUMAN
Primary accession number	P45379
Secondary accession numbers	Q99596 Q99597 O60214
Entered in SWISS-PROT in	Release 32, November 1995
Sequence was last modified in	Release 41, June 2002
Annotations were last modified in	Release 41, June 2002

Name and origin of the protein

Protein name	Troponin T, cardiac muscle isoforms
Synonym	TnTC
Gene name	TNNT2
From	Homo sapiens (Human) [TaxID: 9606]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

References

- [1] SEQUENCE FROM NUCLEIC ACID (ISOFORM 6).
TISSUE=Heart;
MEDLINE=93345675; PubMed=8344420; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
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TISSUE=Fetal heart;
MEDLINE=96129582; PubMed=8576938; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
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"A rapid protocol for cardiac troponin T gene mutation detection in familial hypertrophic cardiomyopathy.";
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TISSUE=Blood;
Farza H., Townsend P.J.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.

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TISSUE=Heart;
MEDLINE=96007936; PubMed=7498159; [NCBI, ExPASy, EBI, Israel, Japan]
Kovalyov L.I., Shishkin S.S., Efimochkin A.S., Kovalyova M.A., Ershova E.S., Egorov T.A.,
Musalyamov A.K.;
"The major protein expression profile and two-dimensional protein database of human heart.";
Electrophoresis 16:1160-1169(1995).

[10] VARIANTS FHC ASN-88 AND GLN-101.
MEDLINE=94265260; PubMed=8205619; [NCBI, ExPASy, EBI, Israel, Japan]
Thierfelder L., Watkins H., Macrae C., Lamas R., McKenna W., Vosberg H.-P., Seidman J.G.,
Seidman C.E.;
"Alpha-tropomyosin and cardiac troponin T mutations cause familial hypertrophic cardiomyopathy: a disease of the sarcomere.";
Cell 77:701-712(1994).

[11] VARIANTS FHC.

MEDLINE=95206332; PubMed=7898523; [NCBI, ExPASy, EBI, Israel, Japan]
Watkins H., McKenna W.J., Thierfelder L., Suk H.J., Anan R., O'Donoghue A., Spirito P.,
Matsumori A., Moravec C.S., Seidman J.G., Seidman C.E.;
 "Mutations in the genes for cardiac troponin T and alpha-tropomyosin in hypertrophic cardiomyopathy.";
New Engl. J. Med. 332:1058-1064(1995).

[12] VARIANT FHC PRO-287.

Erdmann J., Wischke S., Kallisch H., Riedel K., Heidenreich M., Fleck E., Regitz-Zagrosek V.;
 "A novel missense Arg 278 Pro mutation in the troponin T gene (TNNT2).";
Hum. Mutat. 12:364-364(1998).

[13] VARIANT FHC LEU-103.

MEDLINE=99457222; PubMed=10525521; [NCBI, ExPASy, EBI, Israel, Japan]
Varnava A., Baboonian C., Davison F., de Cruz L., Elliott P.M., Davies M.J., McKenna W.J.;
 "A new mutation of the cardiac troponin T gene causing familial hypertrophic cardiomyopathy without left ventricular hypertrophy.";
Heart 82:621-624(1999).

Comments

- **FUNCTION:** TROPONIN T IS THE TROPOMYOSIN-BINDING SUBUNIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFFERS CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
- **ALTERNATIVE PRODUCTS:** At least 10 isoforms; isoform 1/TNT1 (shown here), 2, 3, 4, 5, 6/TNT3, 7/TNT4, 8/TNT2, 9 and 10; may be produced by alternative splicing.
- **TISSUE SPECIFICITY:** Heart. The fetal heart shows a greater expression in the atrium than in the ventricle, while the adult heart shows a greater expression in the ventricle than in the atrium. Isoform 6 predominates in normal adult heart. Isoforms 1, 7 and 8 are expressed in fetal heart. Isoform 7 is also expressed in failing adult heart.
- **DISEASE:** DEFECTS IN TNNT2 ARE ONE OF THE CAUSES OF FAMILIAL HYPERTROPHIC CARDIOMYOPATHY (FHC) WHICH IS AN AUTOSOMAL DOMINANT DISORDER CHARACTERIZED BY INCREASED MYOCARDIAL MASS WITH MYOCYTE AND MYOFIBRILLAR DISARRAY. THIS FORM OF FHC IS KNOWN AS CMH2. IT IS A DISEASE OF THE SARCOMERE.
- **SIMILARITY:** BELONGS TO THE TROPONIN T FAMILY.

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Cross-references

S64668; AAB27731.1; ALT_SEQ.	[EMBL / GenBank / DDBJ] [CoDingSequence]
X74819; CAA52818.1; -.	[EMBL / GenBank / DDBJ] [CoDingSequence]
L40162; AAA67422.1; -.	[EMBL / GenBank / DDBJ] [CoDingSequence]
X79855; CAA56235.1; -.	[EMBL / GenBank / DDBJ] [CoDingSequence]
X79856; CAA56236.1; -.	[EMBL / GenBank / DDBJ] [CoDingSequence]
X79857; CAA56237.1; -.	[EMBL / GenBank / DDBJ] [CoDingSequence]
X79858; CAA56238.1; -.	[EMBL / GenBank / DDBJ] [CoDingSequence]
Y09626; CAA70839.1; -.	[EMBL / GenBank / DDBJ] [CoDingSequence]
Y09627; CAA70840.1; -.	[EMBL / GenBank / DDBJ] [CoDingSequence]
Y09628; CAA70841.1; -.	[EMBL / GenBank / DDBJ] [CoDingSequence]
AF004422; AAC39590.1; -.	[EMBL / GenBank / DDBJ] [CoDingSequence]

	AF004409; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AF004410; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AF004411; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AF004412; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AF004413; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AF004414; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AF004415; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AF004416; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
EMBL	AF004417; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AF004418; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AF004419; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AF004420; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AF004421; AAC39590.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AY044273; AAK92231.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	S71128; AAB30957.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	S71127; AAB30957.1; JOINED. [EMBL / GenBank / DDBJ] [CoDingSequence]
Genew	<u>HGNC:11949</u> ; <u>TNNT2</u> .
MIM	191045 [<u>NCBI / EBI</u>].
	115195 [<u>NCBI / EBI</u>].
GeneCards	<u>TNNT2</u> .
GeneLynx	<u>TNNT2</u> .
SOURCE	<u>TNNT2; Homo sapiens</u> .
Ensembl	P45379; Homo sapiens. [<u>Entry</u> / <u>Contig view</u>]
InterPro	<u>IPR001978; Troponin</u> . <u>Graphical view of domain structure</u> .
Pfam	<u>PF00992; Troponin; 1</u> .
ProDom	[<u>Domain structure</u> / <u>List of seq. sharing at least 1 domain</u>].
BLOCKS	<u>P45379</u> .
ProtoNet	<u>P45379</u> .
ProtoMap	<u>P45379</u> .
PRESAGE	<u>P45379</u> .
DIP	<u>P45379</u> .
ModBase	<u>P45379</u> .

SWISS-2DPAGE GET REGION ON 2D PAGE.**Keywords**

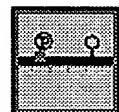
Muscle protein; Alternative splicing; Multigene family; Phosphorylation; Disease mutation; Polymorphism; Cardiomyopathy.

Features

Key	From	To	Length	Description
INIT_MET	0	0		
MOD_RES	<u>1</u>	<u>1</u>		PHOSPHORYLATION (BY CK2) (BY SIMILARITY).
VARSPLIC	<u>17</u>	<u>21</u>		MISSING (IN <u>ISOFORM 8</u>).
VARSPLIC	<u>17</u>	<u>31</u>		MISSING (IN <u>ISOFORM 7</u>).
VARSPLIC	<u>22</u>	<u>31</u>		MISSING (IN <u>ISOFORM 6</u>).
VARSPLIC	<u>22</u>	<u>22</u>		MISSING (IN <u>ISOFORM 2</u> AND <u>ISOFORM 4</u>).
VARSPLIC	<u>53</u>	<u>53</u>		MISSING (IN <u>ISOFORM 3</u> AND

ISOFORM 4).

VARSPLIC	98	136	MISSING (IN <u>ISOFORM 9</u>).
VARSPLIC	200	200	MISSING (IN <u>ISOFORM 5</u>).
VARSPLIC	200	202	MISSING (IN <u>ISOFORM 10</u>).
VARIANT	88	88	I -> N (IN FHC CMH2). /FTId=VAR_007605.
VARIANT	101	101	R -> Q (IN FHC CMH2). /FTId=VAR_007606.
VARIANT	103	103	R -> L (IN FHC CMH2). /FTId=VAR_009194.
VARIANT	119	119	F -> I (IN FHC CMH2). /FTId=VAR_007607.
VARIANT	138	138	R -> K. /FTId=VAR_013021.
VARIANT	169	169	MISSING (IN FHC CMH2). /FTId=VAR_007608.
VARIANT	172	172	E -> K (IN FHC CMH2). /FTId=VAR_007609.
VARIANT	248	248	S -> T. /FTId=VAR_013022.
VARIANT	253	253	E -> D (IN FHC CMH2). /FTId=VAR_007610.
VARIANT	262	262	K -> R. /FTId=VAR_007611.
VARIANT	287	287	R -> C (IN FHC CMH2). /FTId=VAR_007612.
VARIANT	287	287	R -> P (IN FHC CMH2). /FTId=VAR_007613.
CONFLICT	241	241	K -> E (IN REF. <u>8</u>). /FTId=VAR_007614.
CONFLICT	262	262	K -> R (IN REF. <u>8</u>). /FTId=VAR_007615.



Feature table
viewer

Sequence information

Length: 297 Molecular weight: 35792 CRC64: 66FDCCD1EE4A3C965 [This is a checksum on the AA sequence]

10	20	30	40	50	60
SDIEEVVVEEY	EEEEQEEAAAV	EEEEDWREDE	DEQEEAAEED	AEAEAETEET	RAEEDEEEEE
70	80	90	100	110	120
AKEAEDGPME	ESKPKPRSFM	PNLVPPKIPD	GERVDFDDIH	RKRMEEKDLNE	LQALIEAHFE
130	140	150	160	170	180
NRKKKEEEELV	SLKDRIERRR	AERAEQQRIR	NEREKERQNR	LAEERARREE	EENRRKAED
190	200	210	220	230	240
ARKKKALSNM	MHFGGYIQQKQ	AQTERKSGKR	QTEREKKKKI	LAERRKVLA	DHLNEDQLRE
250	260	270	280	290	
KAKELWQSIIY	NLEAEKFDLQ	EKFQQQKYEI	NVLRNRINDN	QKVSKTRGKA	KVTGRWK

P45379 in FASTA
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EMBnet-CH/SIB (Switzerland)



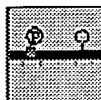
Direct BLAST submission at NCBI (Bethesda, USA)



ScanProsite, MotifScan



Sequence analysis tools: ProtParam, ProtScale,
Compute pI/Mw, PeptideMass, PeptideCutter,
Dotlet (Java)



Feature table viewer (Java)



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